

## P1111

### Genotype Investigator for Genome Wide Analysis (GIGwA)

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Room:

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Comparing genetic variations in relation to the functional data is essential to understand the adaptation of organisms to their ecosystems. However, now with the data deluge produced by the Next Generation Sequencing (NGS) arise some computational challenges regarding storage, search, sharing, analysis, and visualization of data that redefine some practices in data management. In this domain, the traditional relational databases are widely used approaches to store and query data in various forms. However, their major drawback is the lack of flexibility to design the field structures of the data. In addition, relational databases are not efficient to retrieve Gigabytes of data.

In this context, we used the emerging technology called NoSQL for « Not only SQL », which refers to non-relational database management systems designed for large-scale data storage and massively-parallel data processing. GIGwA was mainly developed to manage genomic, transcriptomic and genotyping data from NGS analysis because biologists need to handle large VCF files to filter, query and extract data for their research. However, most of existing tools are mainly targeted at experienced users by providing command line API. The aim of GIGwA is to provide a Web user interface to make the system accessible to users from the biological field.

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### Meeting Information

**When:**

January 10 - 14, 2015

**Where:**

San Diego, CA